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1643

DATE: 09/16/98  
TIME: 16:11:58RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/016,061

INPUT SET: S28676.raw

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APR 21 2000  
TECH CENTER 1600/2800***This Raw Listing contains the General Information Section and up to the first 5 pages.**

## SEQUENCE LISTING

*ENTERED*

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Huse, William D.  
6 Glaser, Scott M.  
7  
8 (ii) TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human  
9 Antibodies, Nucleic Acids Encoding Same and Methods of Use  
10  
11 (iii) NUMBER OF SEQUENCES: 100  
12  
13 (iv) CORRESPONDENCE ADDRESS:  
14 (A) ADDRESSEE: Campbell & Flores LLP  
15 (B) STREET: 4370 La Jolla Village Drive, Suite 700  
16 (C) CITY: San Diego  
17 (D) STATE: California  
18 (E) COUNTRY: United States  
19 (F) ZIP: 92122  
20  
21 (v) COMPUTER READABLE FORM:  
22 (A) MEDIUM TYPE: Floppy disk  
23 (B) COMPUTER: IBM PC compatible  
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
26  
27 (vi) CURRENT APPLICATION DATA:  
28 (A) APPLICATION NUMBER: US 09/016,061  
29 (B) FILING DATE: 30-JAN-1998  
30 (C) CLASSIFICATION:  
31  
32 (vii) PRIOR APPLICATION DATA:  
33 (A) APPLICATION NUMBER: US 08/791,391  
34 (B) FILING DATE: 30-JAN-1997  
35  
36 (viii) ATTORNEY/AGENT INFORMATION:  
37 (A) NAME: Campbell, Cathryn A.  
38 (B) REGISTRATION NUMBER: 31,815  
39 (C) REFERENCE/DOCKET NUMBER: P-IX 2965  
40  
41 (ix) TELECOMMUNICATION INFORMATION:  
42 (A) TELEPHONE: (619) 535-9001  
43 (B) TELEFAX: (619) 535-8949  
44  
45  
46 (2) INFORMATION FOR SEQ ID NO:1:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/016,061DATE: 09/16/98  
TIME: 16:12:00

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47  
48       (i) SEQUENCE CHARACTERISTICS:  
49           (A) LENGTH: 351 base pairs  
50           (B) TYPE: nucleic acid  
51           (C) STRANDEDNESS: both  
52           (D) TOPOLOGY: linear  
53  
54  
55       (ix) FEATURE:  
56           (A) NAME/KEY: CDS  
57           (B) LOCATION: 1..351  
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59  
60       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
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62       CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTT GTG CAG CCT GGA AGG       48  
63       Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
64       1               5               10               15  
65  
66       TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT       96  
67       Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
68       20              25              30  
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70       GAC ATG TCT TGG GTT CGC CAG GCT CCG GGC AAG GGT CTG GAG TGG GTC       144  
71       Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
72       35              40              45  
73  
74       GCA AAA GTT AGT AGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG       192  
75       Ala Lys Val Ser Ser Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val  
76       50              55              60  
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78       CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT AGT AAG AAC ACC CTA TAC       240  
79       Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
80       65              70              75              80  
81  
82       CTG CAA ATG AAC TCT CTG AGA GCC GAG GAC ACA GCC GTG TAT TAC TGT       288  
83       Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
84       85              90              95  
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86       GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT ACA       336  
87       Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr  
88       100             105             110  
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90       GTG ACT GTT TCT AGT    351  
91       Val Thr Val Ser Ser  
92       115  
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95       (2) INFORMATION FOR SEQ ID NO:2:  
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97       (i) SEQUENCE CHARACTERISTICS:  
98           (A) LENGTH: 117 amino acids  
99           (B) TYPE: amino acid

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/016,061**

DATE: 09/16/98  
TIME: 16:12:01

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100                   (D) TOPOLOGY: linear  
 101  
 102                   (ii) MOLECULE TYPE: protein  
 103  
 104                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
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 106       Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
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 108       Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
         20   25                             30  
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 110  
 111       Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
         35   40                             45  
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 114       Ala Lys Val Ser Ser Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val  
         50   55                             60  
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 117       Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
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 120       Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
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 123       Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr  
         100   105                             110  
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 126       Val Thr Val Ser Ser  
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 130       (2) INFORMATION FOR SEQ ID NO:3:  
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 132                   (i) SEQUENCE CHARACTERISTICS:  
 133                      (A) LENGTH: 321 base pairs  
 134                      (B) TYPE: nucleic acid  
 135                      (C) STRANDEDNESS: both  
 136                      (D) TOPOLOGY: linear  
 137  
 138  
 139                   (ix) FEATURE:  
 140                      (A) NAME/KEY: CDS  
 141                      (B) LOCATION: 1..321  
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 144       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
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 146       GAG ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT CTC AGC CCA GGA       48  
 147       Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
         1                         5   10                             15  
 148  
 149  
 150       GAA AGG GCG ACT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC       96  
 151       Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His  
         20   25                             30  
 152

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PATENT APPLICATION US/09/016,061DATE: 09/16/98  
TIME: 16:12:04

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153  
154 CTA CAC TGG TAT CAA CAA AGG CCT GGT CAA GCC CCA AGG CTT CTC ATC 144  
155 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile  
156 35 40 45  
157  
158 AAG TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC GCC AGG TTC AGT GGC 192  
159 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly  
160 50 55 60  
161  
162 AGT GGA TCA GGG ACA GAT TTC ACC CTC ACT ATC TCC AGT CTG GAG CCT 240  
163 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
164 65 70 75 80  
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166 GAA GAT TTT GCA GTC TAT TAC TGT CAA CAG AGT GGC AGC TGG CCT CAC 288  
167 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His  
168 85 90 95  
169  
170 ACG TTC GGA GGG GGG ACC AAG GTG GAA ATT AAG 321  
171 Thr Phe Gly Gly Thr Lys Val Glu Ile Lys  
172 100 105  
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175 (2) INFORMATION FOR SEQ ID NO:4:  
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177 (i) SEQUENCE CHARACTERISTICS:  
178 (A) LENGTH: 107 amino acids  
179 (B) TYPE: amino acid  
180 (D) TOPOLOGY: linear  
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182 (ii) MOLECULE TYPE: protein  
183  
184 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
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186 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
187 1 5 10 15  
188  
189 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His  
190 20 25 30  
191  
192 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile  
193 35 40 45  
194  
195 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly  
196 50 55 60  
197  
198 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
199 65 70 75 80  
200  
201 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His  
202 85 90 95  
203  
204 Thr Phe Gly Gly Thr Lys Val Glu Ile Lys  
205 100 105

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/016,061DATE: 09/16/98  
TIME: 16:12:05

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206  
207 (2) INFORMATION FOR SEQ ID NO:5:  
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209 (i) SEQUENCE CHARACTERISTICS:  
210 (A) LENGTH: 351 base pairs  
211 (B) TYPE: nucleic acid  
212 (C) STRANDEDNESS: both  
213 (D) TOPOLOGY: linear  
214  
215 (ix) FEATURE:  
216 (A) NAME/KEY: CDS  
217 (B) LOCATION: 1..351  
218  
219  
220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
221  
222 GAA GTG CAG CTG GTG GAG TCT GGG GGA GGC TTA GTG AAG CCT GGA AGG 48  
223 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Lys Pro Gly Arg  
224 1 5 10 15  
225  
226 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC GCT TTC AGT AGC TAT 96  
227 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr  
228 20 25 30  
229  
230 GAC ATG TCT TGG GTT CGC CAG ATT CCG GAG AAG AGG CTG GAG TGG GTC 144  
231 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val  
232 35 40 45  
233  
234 GCA AAA GTT AGT AGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG 192  
235 Ala Lys Val Ser Ser Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val  
236 50 55 60  
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238 CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC AAG AAC ACC CTA TAC 240  
239 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr  
240 65 70 75 80  
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242 CTG CAA ATG AGC AGT CTG AAC TCT GAG GAC ACA GCC ATG TAT TAC TGT 288  
243 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys  
244 85 90 95  
245  
246 GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT CTG 336  
247 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu  
248 100 105 110  
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250 GTC ACT GTC TCT GCA 351  
251 Val Thr Val Ser Ala  
252 115  
253  
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255  
256 (2) INFORMATION FOR SEQ ID NO:6:  
257  
258 (i) SEQUENCE CHARACTERISTICS:

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/016,061**

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TIME: 16:12:07

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